

(1) GENERAL INFORMATION:

(i) APPLICANT: Magal, Ella
Delaney, John M.(ii) TITLE OF INVENTION: METHOD FOR PREVENTING AND TREATING
HEARING LOSS USING A NEURTURIN PROTEIN PRODUCT

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Amgen Inc.
(B) STREET: One Amgen Center Drive
(C) CITY: Thousand Oaks
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 91320-1789

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE: 29-JUN-1998
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/054184
(B) FILING DATE: 30-JUL-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Curry, Daniel R.
(B) REGISTRATION NUMBER: 32,727
(C) REFERENCE/DOCKET NUMBER: A-444

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala	Arg	Leu	Gly	Ala	Arg	Pro	Cys	Gly	Leu	Arg	Glu	Leu	Glu	Val	Arg
1				5					10					15	
Val	Ser	Glu	Leu	Gly	Leu	Gly	Tyr	Ala	Ser	Asp	Glu	Thr	Val	Leu	Phe
			20					25					30		
Arg	Tyr	Cys	Ala	Gly	Ala	Cys	Glu	Ala	Ala	Ala	Arg	Val	Tyr	Asp	Leu
		35					40					45			
Gly	Leu	Arg	Arg	Leu	Arg	Gln	Arg	Arg	Arg	Leu	Arg	Arg	Glu	Arg	Val
	50					55					60				

Arg Ala Gln Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser
65 70 75 80

5 Phe Leu Asp Ala His Ser Arg Tyr His Thr Val His Glu Leu Ser Ala
85 90 95

Arg Glu Cys Ala Cys Val
100

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 100 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Pro Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser
1 5 10 15

Glu Leu Gly Leu Gly Tyr Thr Ser Asp Glu Thr Val Leu Phe Arg Tyr
20 25 30

Cys Ala Gly Ala Cys Glu Ala Ala Ile Arg Ile Tyr Asp Leu Gly Leu
35 40 45

Arg Arg Leu Arg Gln Arg Arg Arg Val Arg Arg Glu Arg Ala Arg Ala
50 55 60

His Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu
65 70 75 80

Asp Val His Ser Arg Tyr His Thr Leu Gln Glu Leu Ser Ala Arg Glu
85 90 95

Cys Ala Cys Val
100

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 312 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG GCA CGT CTG GGT GCT CGT CCG TGT GGT CTG CGT GAA CTG GAA GTT
48

Met Ala Arg Leu Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val
65 1 5 10 15

A-444A

- 75 -

5 CGT GTT TCC GAA CTG GGT CTG GGT TAC GCT TCC GAC GAA ACC GTT CTG
96
Arg Val Ser Glu Leu Gly Leu Gly Tyr Ala Ser Asp Glu Thr Val Leu
20 25 30

10 TTC CGT TAC TGT GCA GGT GCT TGT GAA GCA GCT GCA CGT GTT TAC GAC
144
Phe Arg Tyr Cys Ala Gly Ala Cys Glu Ala Ala Ala Arg Val Tyr Asp
35 40 45

15 CTG GGT CTG CGT CGC CTG CGT CAG CGC CGT CGC CTG CGT CGC GAA CGT
192
Leu Gly Leu Arg Arg Leu Arg Gln Arg Arg Arg Leu Arg Arg Glu Arg
50 55 60

20 GTT CGC GCA CAG CCG TGT TGC CGT CCG ACC GCA TAC GAA GAC GAA GTT
240
Val Arg Ala Gln Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val
65 70 75 80

25 TCC TTC CTG GAC GCT CAC TCC CGT TAC CAC ACC GTT CAC GAA CTG TCC
288
Ser Phe Leu Asp Ala His Ser Arg Tyr His Thr Val His Glu Leu Ser
85 90 95

30 GCA CGT CAC TGT GCG TGT GTT TAA
312
Ala Arg His Cys Ala Cys Val
100

(2) INFORMATION FOR SEQ ID NO:4:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

45 Met Ala Arg Leu Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val
1 5 10 15
Arg Val Ser Glu Leu Gly Leu Gly Tyr Ala Ser Asp Glu Thr Val Leu
20 25 30

50 Phe Arg Tyr Cys Ala Gly Ala Cys Glu Ala Ala Ala Arg Val Tyr Asp
35 40 45
Leu Gly Leu Arg Arg Leu Arg Gln Arg Arg Arg Leu Arg Arg Glu Arg
50 55 60

55 Val Arg Ala Gln Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val
65 70 75 80
Ser Phe Leu Asp Ala His Ser Arg Tyr His Thr Val His Glu Leu Ser
85 90 95
Ala Arg His Cys Ala Cys Val
100

65 (2) INFORMATION FOR SEQ ID NO:5:

76

00144-00199

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 197 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

15	Met	Gln	Arg	Trp	Lys	Ala	Ala	Ala	Leu	Ala	Ser	Val	Leu	Cys	Ser	Ser
	1				5					10					15	
	Val	Leu	Ser	Ile	Trp	Met	Cys	Arg	Glu	Gly	Leu	Leu	Leu	Ser	His	Arg
				20					25					30		
20	Leu	Gly	Pro	Ala	Leu	Val	Pro	Leu	His	Arg	Leu	Pro	Arg	Thr	Leu	Asp
			35					40					45			
25	Ala	Arg	Ile	Ala	Arg	Leu	Ala	Gln	Tyr	Arg	Ala	Leu	Gln	Gly	Ala	
		50					55					60				
	Pro	Asp	Ala	Met	Glu	Leu	Arg	Glu	Leu	Thr	Pro	Trp	Ala	Gly	Arg	Pro
	65					70					75					80
30	Pro	Gly	Pro	Arg	Arg	Arg	Ala	Gly	Pro	Arg	Arg	Arg	Arg	Ala	Arg	Ala
					85					90					95	
	Arg	Leu	Gly	Ala	Arg	Pro	Cys	Gly	Leu	Arg	Glu	Leu	Glu	Val	Arg	Val
				100					105					110		
35	Ser	Glu	Leu	Gly	Leu	Gly	Tyr	Ala	Ser	Asp	Glu	Thr	Val	Leu	Phe	Arg
			115					120					125			
	Tyr	Cys	Ala	Gly	Ala	Cys	Glu	Ala	Ala	Ala	Arg	Val	Tyr	Asp	Leu	Gly
40		130					135					140				
	Leu	Arg	Arg	Leu	Arg	Gln	Arg	Arg	Arg	Leu	Arg	Arg	Glu	Arg	Val	Arg
	145					150					155					160
45	Ala	Gln	Pro	Cys	Cys	Arg	Pro	Thr	Ala	Tyr	Glu	Asp	Glu	Val	Ser	Phe
					165					170					175	
	Leu	Asp	Ala	His	Ser	Arg	Tyr	His	Thr	Val	His	Glu	Leu	Ser	Ala	Arg
				180					185					190		
50	Glu	Cys	Ala	Cys	Val											
				195												